wherein binding of the first peptide or segment thereof and the second peptide or segment thereof reconstitutes a transcriptional activation protein; and

c) a reporter gene activated under positive transcriptional control of the reconstituted transcriptional activation protein, wherein expression of the reporter gene produces a selected phenotype;

(ii) incubating a test sample with the Saccharomyces cell under conditions suitable to detect the selected phenotype; and

(iii) detecting the ability of the test sample to affect the binding interaction of the peptide binding pair by determining whether the test sample affects the expression of the reporter gene which produces the selected phenotype.

150. The method of claim 149 wherein the Saccharomyces cell further comprises at least one endogenous nucleotide sequence encoding the reporter gene, wherein at least one of the endogenous nucleotide sequences is inactivated by mutation or deletion.

151. The method of claim 149 wherein the peptide binding pair comprises a ligand and a receptor to which the ligand binds.

152. The method of claim 149 wherein the transcriptional activation protein is Gal4, Adr1, Ace1, or VP16.

153. The method of claim 149 wherein at least one of the heterologous fusion proteins is expressed from an autonomously-replicating plasmid.

154. The method of claim 149 wherein the DNA binding domain is a heterologous transcriptional activation protein DNA-binding domain.

155. The method of claim 154 wherein the DNA binding protein is LexA protein.

156. The method of claim 149 wherein the reporter gene is selected from the group consisting of lacZ, a gene encoding green fluorescent protein, and a gene encoding chloramphenicol acetyltransferase.

157. The method of claim 149 wherein the peptide binding pair is other than an antigen and a corresponding antibody.

158. The method of claim 149 wherein the Saccharomyces cell is *Saccharomyces cerevisiae*.

159. A rescue screen for detecting the ability of a test sample to affect the binding interaction of a first peptide and a second peptide of a peptide binding pair, comprising:

(i) culturing at least one Saccharomyces cell, wherein the Saccharomyces cell comprises;

a) a nucleotide sequence encoding a first heterologous fusion protein comprising the first peptide or a segment thereof joined to a transcriptional activation protein DNA binding domain;

b) a nucleotide sequence encoding a second heterologous fusion protein comprising the second peptide or a segment thereof joined to a transcriptional activation protein transcriptional activation domain;

wherein binding of the first peptide or segment thereof and the second peptide or segment thereof reconstitutes a transcriptional activation protein; and

c) a reporter gene activated under positive transcriptional control of the reconstituted transcriptional activation protein, wherein expression of the reporter gene prevents exhibition of a selected phenotype;

(ii) incubating a test sample with the Saccharomyces cell under conditions suitable to detect the selected phenotype; and

(iii) detecting the ability of the test sample to affect the binding interaction of the peptide binding pair by determining whether the test sample affects the expression of the reporter gene which prevents exhibition of the selected phenotype.

160. The method of claim 159 wherein the Saccharomyces cell further comprises at least one endogenous nucleotide sequence selected from the group consisting of a nucleotide sequence encoding the reporter gene, wherein at least one of the endogenous nucleotide sequences is inactivated by mutation or deletion.

161. The method of claim 159 wherein the peptide binding pair comprises a ligand and a receptor for the ligand.

162. The method of claim 159 wherein the transcriptional activation protein is Gal4, Adr1, Ace1, or VP16.

163. The method of claim 159 wherein at least one of the heterologous fusion proteins is expressed from an autonomously-replicating plasmid.

164. The method of claim 159 wherein the DNA binding domain is a heterologous transcriptional activation protein DNA-binding domain.

165. The method of claim 164 wherein the DNA binding protein is LexA protein.

166. The method of claim 159 wherein the reporter gene is selected from the group consisting of a gene that prevents growth on cycloheximide and a gene that prevents growth on canavanine.

167. The method of claim 159 wherein the peptide binding pair is other than an antigen and a corresponding antibody.

168. The method of claim 159 wherein the Saccharomyces cell is Saccharomyces cerevisiae.

169. A rescue screen for detecting the ability of a test sample to affect the binding interaction of a first and second peptide of a peptide binding pair, comprising:

(i) culturing at least one Saccharomyces cell on a selective medium, wherein the Saccharomyces cell comprises:

a) a nucleotide sequence encoding a first heterologous fusion protein comprising the first peptide or a segment thereof joined to a transcriptional activation protein DNA binding domain;

b) a nucleotide sequence encoding a second heterologous fusion protein comprising the second peptide or a segment thereof joined to a transcriptional activation protein transcriptional activation domain;

wherein binding of the first peptide or segment thereof and the second peptide or segment thereof reconstitutes a transcriptional activation protein;

c) a reporter gene activated under positive transcriptional control of the reconstituted transcriptional activation protein, wherein when the reporter gene is expressed the Saccharomyces cell does not grow on the selective medium; and

(ii) incubating a test sample with the Saccharomyces cell; and

(iii) detecting the ability of the test sample to affect the binding interaction of the peptide binding pair by determining whether the test sample affects the expression of the reporter gene which prevents growth of the Saccharomyces cell on the selective medium.

170. The method of claim 169 wherein the Saccharomyces cell further comprises at least one endogenous nucleotide sequence encoding the reporter gene, wherein at least one of the endogenous nucleotide sequences is inactivated by mutation or deletion.

171. The method of claim 169 wherein the peptide binding pair comprises a ligand and a receptor for the ligand.

172. The method of claim 169 wherein the transcriptional activation protein is Gal4, Adr1, Ace1, or VP16.

173. The method of claim 169 wherein at least one of the heterologous fusion proteins is expressed from an autonomously-replicating plasmid.

174. The method of claim 169 wherein the DNA binding domain is a heterologous transcriptional activation protein DNA-binding domain.

175. The method of claim 174 wherein the DNA binding protein is LexA protein.

176. The method of claim 169 wherein the peptide binding pair is other than an antigen and a corresponding antibody.

177. The method of claim 169 wherein the Saccharomyces cell is *Saccharomyces cerevisiae*.

178. The method of claim 149, wherein the extracellular interaction is between a vins and a hist cell.

179. The method of claim 149, wherein the extracellular interaction is between an antibody and an antigen.

180. The method of claim 149, wherein the extracellular interaction is between a receptor and a signal.

181. A method of detecting the ability of a test compound to affect the binding interaction of a first peptide and a second peptide of a peptide binding pair, the peptide binding pair interacting in an antigen-antibody interaction, a virus-host cell interaction, or a receptor-ligand interaction, the method comprising:

(i) culturing at least one Saccharomyces cell, wherein the cell comprises:

a) a nucleotide sequence encoding a first heterologous fusion protein comprising the first peptide or a segment thereof covalently bonded to a DNA-binding moiety which specifically binds to a DNA-binding-protein recognition site;

b) a nucleotide sequence encoding a second fusion protein expressing a hybrid protein comprising the second peptide or a segment thereof covalently bonded to a gene activating moiety;

wherein binding of the first peptide or segment thereof and the second peptide or segment thereof in the absence of the test compound reconstitutes a transcriptional activation protein; and

c) a reporter gene activated under positive transcriptional control of the reconstituted transcriptional activation protein, wherein expression of the reporter gene produces a selected phenotype;

(ii) incubating a test compound with the cell under conditions suitable to detect the selected phenotype; and

(iii) detecting the ability of the test sample to affect the binding interaction of the peptide binding pair by determining whether the test sample affects the expression of the reporter gene which produces the selected phenotype.

182. The method of claim 181, wherein the Saccharomyces cell further comprises at least one nucleotide sequence encoding the reporter gene, wherein at least one of the endogenous nucleotide sequences is inactivated by mutation or deletion.

183. The method of claim 181, wherein the transcriptional activation protein is Gal4, Adr1, Ace1, or VP16.

184. The method of claim 181, wherein at least one of the heterologous fusion proteins is expressed from an autonomously-replicating plasmid.

185. The method of claim 181, wherein the DNA binding domain is a heterologous transcriptional activation protein DNA-binding domain.

186. The method of claim 185, wherein the DNA binding protein is LexA protein.

187. The method of claim 181, wherein the reporter gene is selected from the group consisting of lacZ, a gene encoding green fluorescent protein, and a gene encoding chloramphenicol acetyltransferase.

188. The method of claim 181 wherein the peptide binding pair is other than an antigen and a corresponding antibody.

189. The method of claim 181, wherein the Saccharomyces cell is *Saccharomyces cerevisiae*.

190. A method of detecting the ability of a test compound to affect the binding interaction of a first peptide and a second peptide of a peptide binding pair, comprising:

(i) culturing at least one Saccharomyces cell, wherein the cell comprises;

a) a nucleotide sequence encoding a first heterologous fusion protein comprising the first peptide or a segment thereof covalently bonded to a DNA-binding moiety which specifically binds to a DNA-binding-protein recognition site;

b) a nucleotide sequence encoding a second heterologous fusion protein comprising the second peptide or a segment thereof covalently bonded to gene activating moiety;

wherein binding of the first peptide or segment thereof and the second peptide or segment thereof reconstitutes a transcriptional activation protein; and

c) a counterselectable reporter gene operably linked to the DNA-binding-protein recognition site, wherein expression of the reporter gene prevents exhibition of a selected phenotype;

(ii) incubating a test compound with the Saccharomyces cell under conditions suitable to detect the selected phenotype; and

(iii) detecting the ability of the test compound to affect the binding interaction of the peptide binding pair by determining whether the test compound affects the expression of the reporter gene which prevents exhibition of the selected phenotype.

191. The method of claim 190, wherein the Saccharomyces cell further comprises at least one endogenous nucleotide sequence encoding the reporter gene, wherein at least one of the endogenous nucleotide sequences is inactivated by mutation or deletion.

192. The method of claim 190, wherein the peptide binding pair comprises a ligand and a receptor for the ligand.

193. The method of claim 190, wherein the transcriptional activation protein is Gal4, Adr1, Ace1, or VP16.

194. The method of claim 190, wherein at least one of the heterologous fusion proteins is expressed from an autonomously-replicating plasmid.

195. The method of claim 190, wherein the DNA binding domain is a heterologous transcriptional activation protein DNA-binding domain.

196. The method of claim 195, wherein the DNA binding protein is LexA protein.

197. The method of claim 190, wherein the reporter gene is selected from the group consisting of a gene that prevents growth on cycloheximide and a gene that prevents growth on canavanine.

198. The method of claim 190, wherein the peptide binding pair is other than an antigen and a corresponding antibody.

199. The method of claim 190, wherein the Saccharomyces cell is *Saccharomyces cerevisiae*.

200. A method for detecting the ability of a test compound to affect the binding interaction of a first and second peptide of a peptide binding pair, comprising:

(i) culturing at least one cell on a selective medium, wherein the cell comprises;

a) a nucleotide sequence encoding a first heterologous fusion protein comprising the first peptide or a segment thereof covalently bonded to a DNA-binding moiety which specifically binds to a DNA-binding-protein recognition site;

b) a nucleotide sequence encoding a second heterologous fusion protein comprising the second peptide or a segment thereof covalently bonded to a gene activating moiety;

wherein binding of the first peptide or segment thereof and the second peptide or segment thereof reconstitutes a transcriptional activation protein;

c) a counterselectable reporter gene activated under positive transcriptional control of the reconstituted transcriptional activation protein, wherein when the reporter gene is expressed the cell does not grow on the selective medium; and

(ii) incubating a test compound with the cell; and

(iii) detecting the ability of the test compound to affect the binding interaction of the peptide binding pair by determining whether the test compound affects the expression of the reporter gene which prevents growth of the cell on the selective medium.

201. The method of claim 200, wherein the cell is a Saccharomyces cell.

202. The method of claim 200, wherein the cell further comprises at least one endogenous nucleotide sequence encoding the reporter gene, wherein at least one of the endogenous nucleotide sequences is inactivated by mutation or deletion.

203. The method of claim 200, wherein the peptide binding pair comprises a ligand and a receptor for the ligand.

204. The method of claim 200 wherein the transcriptional activation protein is Gal4, Adr1, Ace1, or VP16.

205. The method of claim 200, wherein at least one of the heterologous fusion proteins is expressed from an autonomously-replicating plasmid.

206. The method of claim 200, wherein the DNA binding domain is a heterologous transcriptional activation protein DNA-binding domain.

207. The method of claim 206, wherein the DNA binding protein is bacterial LexA protein.

208. The method of claim 200, wherein the peptide binding pair is other than an antigen and a corresponding antibody.

209. The method of claim 200, wherein the Saccharomyces cell is *Saccharomyces cerevisiae*.

210. A method for determining whether a test compound disrupts binding between a first test protein and a second test protein, said method comprising:

(a) providing a Saccharomyces cell containing:

(i) a counterselectable reporter gene operably linked to a DNA-binding-protein recognition site;

(ii) a first fusion gene expressing a first hybrid protein comprising said first test protein covalently bonded to a DNA-binding moiety which is capable of specifically binding to said DNA-binding-protein recognition site; and

(iii) a second fusion gene expressing a second hybrid protein comprising said second test protein covalently bonded to a gene activating moiety, wherein said second test protein binds said first test protein in the absence of said test compound;